



## SEQUENCE LISTING

<110> Stashenko, Philip  
 Okamatsu, Yoshimura  
 Sasaki, Hajime  
 Battaglino, Richard  
 Spaete, Ulrike

<120> Expressed Genes that Define the Osteoclast Phenotype

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<140> 10/734,692  
 <141> 2003-12-11

<150> 60/432,700  
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<170> PatentIn version 3.2

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Gly Ala Gln Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe Val Ile Gly
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Leu Val Gly Asn Ile Leu Val Val Leu Val Leu Val Gln Tyr Lys Arg
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Leu Lys Asn Met Thr Ser Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp
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Val Leu Pro Leu Leu Val Met Ile Ile Cys Tyr Thr Gly Ile Ile Lys  
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Cys Glu Gln Ser Arg His Leu Asp Leu Ala Val Gln Val Thr Glu Val  
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Ile Ala Tyr Thr His Cys Cys Val Asn Pro Val Ile Tyr Ala Phe Val  
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Gly Glu Arg Phe Arg Lys Tyr Leu Arg Gln Leu Phe His Arg Arg Val  
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35          40          45

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Leu Lys Asn Met Thr Ser Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp  
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Leu Leu Phe Leu Phe Thr Leu Pro Phe Trp Ile Asp Tyr Lys Leu Lys  
 85 90 95

Asp Asp Trp Val Phe Gly Asp Ala Met Cys Lys Ile Leu Ser Gly Phe  
 100 105 110

Tyr Tyr Thr Gly Leu Tyr Ser Glu Ile Phe Phe Ile Ile Leu Leu Thr  
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Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Arg Ala  
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Arg Thr Val Thr Phe Gly Val Ile Thr Ser Ile Ile Ile Trp Ala Leu  
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Ala Ile Leu Ala Ser Met Pro Gly Leu Tyr Phe Ser Lys Thr Gln Trp  
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Glu Phe Thr His His Thr Cys Ser Leu His Phe Pro His Glu Ser Leu  
 180 185 190

Arg Glu Trp Lys Leu Phe Gln Ala Leu Lys Leu Asn Leu Phe Gly Leu  
 195 200 205

Val Leu Pro Leu Leu Val Met Ile Ile Cys Tyr Thr Gly Ile Ile Lys  
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Ile Leu Leu Arg Arg Pro Asn Glu Lys Lys Ser Lys Ala Val Arg Leu  
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Ile Phe Val Ile Met Ile Ile Phe Phe Leu Phe Trp Thr Pro Tyr Asn  
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Leu Thr Ile Leu Ile Ser Val Phe Gln Asp Phe Leu Phe Thr His Glu  
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Cys Glu Gln Ser Arg His Leu Asp Leu Ala Val Gln Val Thr Glu Val  
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Ile Ala Tyr Thr His Cys Cys Val Asn Pro Val Ile Tyr Ala Phe Val  
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Gly Glu Arg Phe Arg Lys Tyr Leu Arg Gln Leu Phe His Arg Arg Val  
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Ala Val His Leu Val Lys Trp Leu Pro Phe Leu Ser Val Asp Arg Leu  
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gccctcgtct gagaagatcg ccgccatcgc cgagaaactg gacctcaaaa agaacgtggg 2040
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```

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<210> 31
<211> 421
<212> PRT
<213> Mus sp.

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<400> 31

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Met Met Ser Met Asn Ser Lys Gln Pro His Phe Ala Met His Pro Thr
1           5           10          15

```

```

Leu Pro Glu His Lys Tyr Pro Ser Leu His Ser Ser Ser Glu Ala Ile
20           25           30

```

Arg Arg Ala Cys Leu Pro Thr Pro Pro Leu Gln Ser Asn Leu Phe Ala  
 35 40 45

Ser Leu Asp Glu Thr Leu Leu Ala Arg Ala Glu Ala Leu Ala Ala Val  
 50 55 60

Asp Ile Ala Val Ser Gln Gly Lys Ser His Pro Phe Lys Pro Asp Ala  
 65 70 75 80

Thr Tyr His Thr Met Asn Ser Val Pro Cys Thr Ser Thr Ser Thr Val  
 85 90 95

Pro Leu Ala His His His His His His His His His His Gln Ala Leu Glu  
 100 105 110

Pro Gly Asp Leu Leu Asp His Ile Ser Ser Pro Ser Leu Ala Leu Met  
 115 120 125

Ala Gly Ala Gly Gly Ala Gly Ala Ala Gly Gly Gly Gly Gly Ala His  
 130 135 140

Asp Gly Pro Gly Gly Gly Gly Gly Gly Pro Gly Gly Gly Gly Gly Pro Gly  
 145 150 155 160

Gly Gly Gly Pro Gly Gly Gly Gly Gly Gly Gly Gly Gly Pro Gly Gly Gly  
 165 170 175

Gly Gly Ala Pro Gly Gly Gly Leu Leu Gly Gly Ser Ala His Pro His  
 180 185 190

Pro His Met His Gly Leu Gly His Leu Ser His Pro Ala Ala Ala Ala  
 195 200 205

Ala Met Asn Met Pro Ser Gly Leu Pro His Pro Gly Leu Val Ala Ala  
 210 215 220

Ala Ala His His Gly Ala Ala Ala Ala Ala Ala Ala Ala Ala Gly  
 225 230 235 240

Gln Val Ala Ala Ala Ser Ala Ala Ala Ala Val Val Gly Ala Ala Gly  
 245 250 255

Leu Ala Ser Ile Cys Asp Ser Asp Thr Asp Pro Arg Glu Leu Glu Ala  
 260 265 270

Phe Ala Glu Arg Phe Lys Gln Arg Arg Ile Lys Leu Gly Val Thr Gln  
 275 280 285

Ala Asp Val Gly Ser Ala Leu Ala Asn Leu Lys Ile Pro Gly Val Gly  
 290 295 300

Ser Leu Ser Gln Ser Thr Ile Cys Arg Phe Glu Ser Leu Thr Leu Ser  
 305 310 315 320

His Asn Asn Met Ile Ala Leu Lys Pro Ile Leu Gln Ala Trp Leu Glu  
 325 330 335

Glu Ala Glu Gly Ala Gln Arg Glu Lys Met Asn Lys Pro Glu Leu Phe  
 340 345 350

Asn Gly Gly Glu Lys Lys Arg Lys Arg Thr Ser Ile Ala Ala Pro Glu  
 355 360 365

Lys Arg Ser Leu Glu Ala Tyr Phe Ala Val Gln Pro Arg Pro Ser Ser  
 370 375 380

Glu Lys Ile Ala Ala Ile Ala Glu Lys Leu Asp Leu Lys Lys Asn Val  
 385 390 395 400

Val Arg Val Trp Phe Cys Asn Gln Arg Gln Lys Gln Lys Arg Met Lys  
 405 410 415

Phe Ser Ala Thr Tyr  
 420

<210> 32  
 <211> 123  
 <212> DNA  
 <213> Homo sapiens

<400> 32  
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 aagtaccctg cgctgcactc cagctccgag gccatccggc gggcctgcct gccacgccc 120  
 ccg 123



<210> 33  
 <211> 1149  
 <212> DNA  
 <213> Homo sapiens

<400> 33  
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 taccacacga tgaacagcgt gccgtgcacg tccacttcca cggcgcctct gcggcaccac 180  
 caccaccacc accaccacca ccaggcgctc gaaccggcg atctgctgga ccacatctcc 240  
 tcgccgtcgc tcgcgctcat ggccggcgcg gccggcgcg gcggcgcggg cgccggcgggc 300  
 ggccggcgcg gcgcccacga cggcccgggg gccgggtggc gcccgggcg cgccggcgggc 360  
 ccggcgcgcg gcggcccgcg gggaggcggc ggtggcgggc cggggggcg cgccggcgggc 420  
 ccggcgcgcg ggctcctggg cggctccgcg caccctcacc cgcataatga cagcctgggc 480  
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 acttactga 1149

<210> 34  
 <211> 423  
 <212> PRT  
 <213> Homo sapiens

<400> 34  
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Leu Pro Glu His Lys Tyr Pro Ser Leu His Ser Ser Ser Glu Ala Ile  
 20, 25 30

Arg Arg Ala Cys Leu Pro Thr Pro Pro Leu Gln Ser Asn Leu Phe Ala  
 35 40 45

Ser Leu Asp Glu Thr Leu Leu Ala Arg Ala Glu Ala Leu Ala Ala Val  
 50 55 60

Asp Ile Ala Val Ser Gln Gly Lys Ser His Pro Phe Lys Pro Asp Ala  
 65 70 75 80

Thr Tyr His Thr Met Asn Ser Val Pro Cys Thr Ser Thr Ser Thr Val  
 85 90 95

Pro Leu Arg His His His His His His His His His His Gln Ala Leu Glu  
 100 105 110

Pro Gly Asp Leu Leu Asp His Ile Ser Ser Pro Ser Leu Ala Leu Met  
 115 120 125

Ala Gly Ala Gly Gly Ala Gly Gly Ala Gly Ala Ala Ala Gly Gly Gly  
 130 135 140

Gly Ala His Asp Gly Pro Gly Gly Gly Gly Gly Gly Pro Gly Gly Gly Gly  
 145 150 155 160

Gly Pro Gly Gly Gly Gly Pro Gly Gly Gly Gly Gly Gly Gly Gly Pro Gly  
 165 170 175

Gly Gly Gly Gly Gly Pro Gly Gly Gly Leu Leu Gly Gly Ser Ala His  
 180 185 190

Pro His Pro His Met His Ser Leu Gly His Leu Ser His Pro Ala Ala  
 195 200 205

Ala Ala Ala Met Asn Met Pro Ser Gly Leu Pro His Pro Gly Leu Val  
 210 215 220

Ala Ala Ala Ala His His Gly Ala Ala Ala Ala Ala Ala Ala Ala Ala  
 225 230 235 240

Ala Gly Gln Val Ala Ala Ala Ser Ala Ala Ala Ala Val Val Gly Ala  
245 250 255

Ala Gly Leu Ala Ser Ile Cys Asp Ser Asp Thr Asp Pro Arg Glu Leu  
260 265 270

Glu Ala Phe Ala Glu Arg Phe Lys Gln Arg Arg Ile Lys Leu Gly Val  
275 280 285

Thr Gln Ala Asp Val Gly Ser Ala Leu Ala Asn Leu Lys Ile Pro Gly  
290 295 300

Val Gly Ser Leu Ser Gln Ser Thr Ile Cys Arg Phe Glu Ser Leu Thr  
305 310 315 320

Leu Ser His Asn Asn Met Ile Ala Leu Lys Pro Ile Leu Gln Ala Trp  
325 330 335

Leu Glu Glu Ala Glu Gly Ala Gln Arg Glu Lys Met Asn Lys Pro Glu  
340 345 350

Leu Phe Asn Gly Gly Glu Lys Lys Arg Lys Arg Thr Ser Ile Ala Ala  
355 360 365

Pro Glu Lys Arg Ser Leu Glu Ala Tyr Phe Ala Val Gln Pro Arg Pro  
370 375 380

Ser Ser Glu Lys Ile Ala Ala Ile Ala Glu Lys Leu Asp Leu Lys Lys  
385 390 395 400

Asn Val Val Arg Val Trp Phe Cys Asn Gln Arg Gln Lys Gln Lys Arg  
405 410 415

Met Lys Phe Ser Ala Thr Tyr  
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<210> 35

<211> 1091

<212> DNA

<213> Mus musculus

<400> 35

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 tgctggcccc tgccgagget ctggccgccg tggacatcgt ctcccagagt aagagccacc 240  
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 ccatcccgtg cacgtcggca gcctcctctt cttctgtgcc catctcgcac ccgtccgctc 360  
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 ccggcattta g 1091

<210> 36

<211> 322

<212> PRT

<213> Mus musculus

<400> 36

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Asp Glu Ser Leu Leu Ala Arg Ala Glu Ala Leu Ala Ala Val Asp Ile  
 20 25 30

Val Ser Gln Ser Lys Ser His His His His Pro Pro His His Ser Pro  
 35 40 45

Phe Lys Pro Asp Ala Thr Tyr His Thr Met Asn Thr Ile Pro Cys Thr

50		55		60											
Ser	Ala	Ala	Ser	Ser	Ser	Ser	Val	Pro	Ile	Ser	His	Pro	Ser	Ala	Leu
65					70					75					80
Ala	Gly	Thr	His	His	His	His	His	His	His	His	His	His	His	His	Gln
			85					90						95	
Pro	His	Gln	Ala	Leu	Glu	Gly	Glu	Leu	Leu	Glu	His	Leu	Ser	Pro	Gly
			100					105					110		
Leu	Ala	Leu	Gly	Ala	Met	Ala	Gly	Pro	Asp	Gly	Thr	Val	Val	Ser	Thr
		115					120					125			
Pro	Ala	His	Ala	Pro	His	Met	Ala	Thr	Met	Asn	Pro	Met	His	Gln	Ala
		130				135					140				
Ala	Leu	Ser	Met	Ala	His	Ala	His	Gly	Leu	Pro	Ser	His	Met	Gly	Cys
145					150					155					160
Met	Ser	Asp	Val	Asp	Ala	Asp	Pro	Arg	Asp	Leu	Glu	Ala	Phe	Ala	Glu
				165					170					175	
Arg	Phe	Lys	Gln	Arg	Arg	Ile	Lys	Leu	Gly	Val	Thr	Gln	Ala	Asp	Val
			180					185						190	
Gly	Ser	Ala	Leu	Ala	Asn	Leu	Lys	Ile	Pro	Gly	Val	Gly	Ser	Leu	Ser
		195					200					205			
Gln	Ser	Thr	Ile	Cys	Arg	Phe	Glu	Ser	Leu	Thr	Leu	Ser	His	Asn	Asn
		210				215					220				
Met	Ile	Ala	Leu	Lys	Pro	Ile	Leu	Gln	Ala	Trp	Leu	Glu	Glu	Ala	Glu
225					230					235					240
Lys	Ser	His	Arg	Glu	Lys	Leu	Thr	Lys	Pro	Glu	Leu	Phe	Asn	Gly	Ala
				245					250					255	
Glu	Lys	Lys	Arg	Lys	Arg	Thr	Ser	Ile	Ala	Ala	Pro	Glu	Lys	Arg	Ser
			260					265					270		
Leu	Glu	Ala	Tyr	Phe	Ala	Ile	Gln	Pro	Arg	Pro	Ser	Ser	Glu	Lys	Ile
		275					280					285			

Ala Ala Ile Ala Glu Lys Leu Asp Leu Lys Lys Asn Val Val Arg Val  
 290 295 300

Trp Phe Cys Asn Gln Arg Gln Lys Gln Lys Lys Val Lys Tyr Ser Ala  
 305 310 315 320

Gly Ile

<210> 37  
 <211> 3110  
 <212> DNA  
 <213> Homo sapiens

<400> 37  
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 ctctacggac cagcgcccccg gcgggcggga agatgatgat gatgtccctg aacagcaagc 240  
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 acagcacctc gccggggtcc tcgggtccca tcgcgcctc ggccagctcc ccagcagct 360  
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tattatatat atatttttat tgtggttctt accccctttt ctttctctga agtgttaatg	2040
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cctctaacag aaggggaagaa gcagttggaa gcatgaccga tgcaccattt tctagtttta	2580
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actggtacct tatctactgt aaatatttca ttaaaaatga tgcacacata gatatatctt 2880
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<210> 38
<211> 410
<212> PRT
<213> Homo sapiens

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<400> 38

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Met Met Met Met Ser Leu Asn Ser Lys Gln Ala Phe Ser Met Pro His
1             5             10             15

```

```

Gly Gly Ser Leu His Val Glu Pro Lys Tyr Ser Ala Leu His Ser Thr
20             25             30

```

```

Ser Pro Gly Ser Ser Ala Pro Ile Ala Pro Ser Ala Ser Ser Pro Ser
35             40             45

```

```

Ser Ser Ser Asn Ala Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
50             55             60

```

```

Gly Gly Gly Gly Gly Arg Ser Ser Ser Ser Ser Ser Ser Gly Ser Ser
65             70             75             80

```

```

Gly Gly Gly Gly Ser Glu Ala Met Arg Arg Ala Cys Leu Pro Thr Pro
85             90             95

```

```

Pro Ser Asn Ile Phe Gly Gly Leu Asp Glu Ser Leu Leu Ala Arg Ala
100            105            110

```

```

Glu Ala Leu Ala Ala Val Asp Ile Val Ser Gln Ser Lys Ser His His
115            120            125

```

```

His His Pro Pro His His Ser Pro Phe Lys Pro Asp Ala Thr Tyr His
130            135            140

```

```

Thr Met Asn Thr Ile Pro Cys Thr Ser Ala Ala Ser Ser Ser Ser Val
145            150            155            160

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Pro Ile Ser His Pro Cys Ala Leu Ala Gly Thr His His His His His  
 165 170 175

His His His His His His His Gln Pro His Gln Ala Leu Glu Gly Glu  
 180 185 190

Leu Leu Glu His Leu Ser Pro Gly Leu Ala Leu Gly Ala Met Ala Gly  
 195 200 205

Pro Asp Gly Ala Val Val Ser Thr Pro Ala His Ala Pro His Met Ala  
 210 215 220

Thr Met Asn Pro Met His Gln Ala Ala Leu Ser Met Ala His Ala His  
 225 230 235 240

Gly Leu Pro Ser His Met Gly Cys Met Ser Asp Val Asp Ala Asp Pro  
 245 250 255

Arg Asp Leu Glu Ala Phe Ala Glu Arg Phe Lys Gln Arg Arg Ile Lys  
 260 265 270

Leu Gly Val Thr Gln Ala Asp Val Gly Ser Ala Leu Ala Asn Leu Lys  
 275 280 285

Ile Pro Gly Val Gly Ser Leu Ser Gln Ser Thr Ile Cys Arg Phe Glu  
 290 295 300

Ser Leu Thr Leu Ser His Asn Asn Met Ile Ala Leu Lys Pro Ile Leu  
 305 310 315 320

Gln Ala Trp Leu Glu Glu Ala Glu Lys Ser His Arg Glu Lys Leu Thr  
 325 330 335

Lys Pro Glu Leu Phe Asn Gly Ala Glu Lys Lys Arg Lys Arg Thr Ser  
 340 345 350

Ile Ala Ala Pro Glu Lys Arg Ser Leu Glu Ala Tyr Phe Ala Ile Gln  
 355 360 365

Pro Arg Pro Ser Ser Glu Lys Ile Ala Ala Ile Ala Glu Lys Leu Asp  
 370 375 380

Leu Lys Lys Asn Val Val Arg Val Trp Phe Cys Asn Gln Arg Gln Lys  
 385 390 395 400

Gln Lys Arg Met Lys Tyr Ser Ala Gly Ile  
 405 410

<210> 39  
 <211> 1594  
 <212> DNA  
 <213> Mus musculus

<400> 39  
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 tggccatgaa cgccaagcac cgtttcggca tgcaccccgt actgcaagaa cccaaattct 180  
 ccagcctaca ctccggctct gaggccatgc gccgagtttg tctcccagcc ccgcaggtac 240  
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 cctgcacttc tacctcgccc acggtgcccc tctctcaccg ggctgcactc acctcgacc 780  
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 agaaacagaa acgaatgaaa tactctgctg tggactgatt gcggcgggtg ctgcgtccgg 1500  
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<210> 40  
 <211> 338  
 <212> PRT  
 <213> Mus musculus

<400> 40

Met Met Ala Met Asn Ala Lys His Arg Phe Gly Met His Pro Val Leu  
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Gln Glu Pro Lys Phe Ser Ser Leu His Ser Gly Ser Glu Ala Met Arg  
 20 25 30

Arg Val Cys Leu Pro Ala Pro Gln Leu Gln Gly Asn Ile Phe Gly Ser  
 35 40 45

Phe Asp Glu Ser Leu Leu Ala Arg Ala Glu Ala Leu Ala Ala Val Asp  
 50 55 60

Ile Val Ser His Gly Lys Asn His Pro Phe Lys Pro Asp Ala Thr Tyr  
 65 70 75 80

His Thr Met Ser Ser Val Pro Cys Thr Ser Thr Ser Pro Thr Val Pro  
 85 90 95

Ile Ser His Pro Ala Ala Leu Thr Ser His Pro His His Ala Val His  
 100 105 110

Gln Gly Leu Glu Gly Asp Leu Leu Glu His Ile Ser Pro Thr Leu Ser  
 115 120 125

Val Ser Gly Leu Gly Ala Pro Glu His Ser Val Met Pro Ala Gln Ile  
 130 135 140

His Pro His His Leu Gly Ala Met Gly His Leu His Gln Ala Met Gly  
 145 150 155 160

Met Ser His Pro His Ala Val Ala Pro His Ser Ala Met Pro Ala Cys  
165 170 175

Leu Ser Asp Val Glu Ser Asp Pro Arg Glu Leu Glu Ala Phe Ala Glu  
180 185 190

Arg Phe Lys Gln Arg Arg Ile Lys Leu Gly Val Thr Gln Ala Asp Val  
195 200 205

Gly Ala Ala Leu Ala Asn Leu Lys Ile Pro Gly Val Gly Ser Leu Ser  
210 215 220

Gln Ser Thr Ile Cys Arg Phe Glu Ser Leu Thr Leu Ser His Asn Asn  
225 230 235 240

Met Ile Ala Leu Lys Pro Val Leu Gln Ala Trp Leu Glu Glu Ala Glu  
245 250 255

Ala Ala Tyr Arg Glu Lys Asn Ser Lys Pro Glu Leu Phe Asn Gly Ser  
260 265 270

Glu Arg Lys Arg Lys Arg Thr Ser Ile Ala Ala Pro Glu Lys Arg Ser  
275 280 285

Leu Glu Ala Tyr Phe Ala Ile Gln Pro Arg Pro Ser Ser Glu Lys Ile  
290 295 300

Ala Ala Ile Ala Glu Lys Leu Asp Leu Lys Lys Asn Val Val Arg Val  
305 310 315 320

Trp Phe Cys Asn Gln Arg Gln Lys Gln Lys Arg Met Lys Tyr Ser Ala  
325 330 335

Val Asp

<210> 41  
<211> 120  
<212> DNA  
<213> Homo sapiens

<400> 41  
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60

ttctccagtc tgcactctgg ctccgaggct atgcgccgag tctgtctccc agccccgcag 120

<210> 42  
 <211> 897  
 <212> DNA  
 <213> Homo sapiens

<400> 42  
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 gcggcggtgg atatcgtctc ccacggcaag aaccatccgt tcaagcccga cgccacctac 120  
 cataccatga gcagcgtgcc ctgcacgtcc acttcgtcca ccgtgcccac ctcccaccca 180  
 gctgcgctca cctcacaccc tcaccacgcc gtgcaccagg gcctcgaagg cgacctgctg 240  
 gagcacatct cgcccacgct gagggtgagc ggccctgggcg ctccggaaca ctcggtgatg 300  
 cccgcacaga tccatccaca ccacctgggc gccatgggccc acctgcacca ggccatgggc 360  
 atgagtcacc cgcacaccgt ggcccctcat agcgccatgc ctgcatgcct cagcgacgtg 420  
 gaggcagacc cgcgcgagct ggaagccttc gccgagcgct tcaagcagcg gcgcatcaag 480  
 ctggggggtga cccaggcgga cgtgggcgcg gctctggcta atctcaagat ccccggcgtg 540  
 ggctcgctga gccaaagcac catctgcagg ttcgagtctc tcaactctctc gcacaacaac 600  
 atgatcgctc tcaagccggt gctccaggcc tgggtggagg aggccgaggc cgcctaccga 660  
 gagaagaaca gcaagccaga gctcttcaac ggacgcgaac ggaagcgcaa acgcacgtcc 720  
 atcgcggcgc cggagaagcg ttcactcgag gcctatttcg ctatccagcc acgtccttca 780  
 tctgagaaga tcgcggccat cgctgagaaa ctggacctta aaaagaacgt ggtgagagtc 840  
 tggttctgca accagagaca gaaacagaaa cgaatgaagt attcggtgtt cactga 897

<210> 43  
 <211> 338  
 <212> PRT  
 <213> Homo sapiens

<400> 43

Met Met Ala Met Asn Ser Lys Gln Pro Phe Gly Met His Pro Val Leu  
 1 5 10 15

Gln Glu Pro Lys Phe Ser Ser Leu His Ser Gly Ser Glu Ala Met Arg  
 20 25 30

Arg Val Cys Leu Pro Ala Pro Gln Leu Gln Gly Asn Ile Phe Gly Ser

35																	
Phe	Asp	Glu	Ser	Leu	Leu	Ala	Arg	Ala	Glu	Ala	Leu	Ala	Ala	Val	Asp		
50						55					60						
Ile	Val	Ser	His	Gly	Lys	Asn	His	Pro	Phe	Lys	Pro	Asp	Ala	Thr	Tyr		
65					70					75					80		
His	Thr	Met	Ser	Ser	Val	Pro	Cys	Thr	Ser	Thr	Ser	Ser	Thr	Val	Pro		
				85					90					95			
Ile	Ser	His	Pro	Ala	Ala	Leu	Thr	Ser	His	Pro	His	His	Ala	Val	His		
			100					105					110				
Gln	Gly	Leu	Glu	Gly	Asp	Leu	Leu	Glu	His	Ile	Ser	Pro	Thr	Leu	Ser		
		115					120					125					
Val	Ser	Gly	Leu	Gly	Ala	Pro	Glu	His	Ser	Val	Met	Pro	Ala	Gln	Ile		
	130					135					140						
His	Pro	His	His	Leu	Gly	Ala	Met	Gly	His	Leu	His	Gln	Ala	Met	Gly		
145					150					155					160		
Met	Ser	His	Pro	His	Thr	Val	Ala	Pro	His	Ser	Ala	Met	Pro	Ala	Cys		
				165					170					175			
Leu	Ser	Asp	Val	Glu	Ser	Asp	Pro	Arg	Glu	Leu	Glu	Ala	Phe	Ala	Glu		
			180					185					190				
Arg	Phe	Lys	Gln	Arg	Arg	Ile	Lys	Leu	Gly	Val	Thr	Gln	Ala	Asp	Val		
		195					200					205					
Gly	Ala	Ala	Leu	Ala	Asn	Leu	Lys	Ile	Pro	Gly	Val	Gly	Ser	Leu	Ser		
	210					215					220						
Gln	Ser	Thr	Ile	Cys	Arg	Phe	Glu	Ser	Leu	Thr	Leu	Ser	His	Asn	Asn		
225					230					235					240		
Met	Ile	Ala	Leu	Lys	Pro	Val	Leu	Gln	Ala	Trp	Leu	Glu	Glu	Ala	Glu		
				245					250					255			
Ala	Ala	Tyr	Arg	Glu	Lys	Asn	Ser	Lys	Pro	Glu	Leu	Phe	Asn	Gly	Ser		
			260					265					270				

Glu Arg Lys Arg Lys Arg Thr Ser Ile Ala Ala Pro Glu Lys Arg Ser  
 275 280 285

Leu Glu Ala Tyr Phe Ala Ile Gln Pro Arg Pro Ser Ser Glu Lys Ile  
 290 295 300

Ala Ala Ile Ala Glu Lys Leu Asp Leu Lys Lys Asn Val Val Arg Val  
 305 310 315 320

Trp Phe Cys Asn Gln Arg Gln Lys Gln Lys Arg Met Lys Tyr Ser Ala  
 325 330 335

Val His

<210> 44  
 <211> 18  
 <212> DNA  
 <213> Homo sapiens

<400> 44  
 cacagctcat taacgcgc 18

<210> 45  
 <211> 18  
 <212> DNA  
 <213> Homo sapiens

<400> 45  
 cactcctcat taacgcgc 18

<210> 46  
 <211> 18  
 <212> DNA  
 <213> Homo sapiens

<400> 46  
 cacagctcat taagtcgc 18

<210> 47  
 <211> 18  
 <212> DNA  
 <213> Homo sapiens

<400> 47  
 cacgcatgcg taatgcgc 18

<210> 48  
 <211> 11  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (5)..(7)  
 <223> wherein n is a, c, g, or t

<400> 48  
 gcatnnntaa t 11

<210> 49  
 <211> 11  
 <212> DNA  
 <213> Rattus norvegicus

<400> 49  
 gcataaataa t 11

<210> 50  
 <211> 668  
 <212> DNA  
 <213> Mus musculus

<220>  
 <221> misc\_feature  
 <222> (49)..(49)  
 <223> wherein n is a, c, g, or t

<400> 50  
 tggagcagag gtttccattg tgtctctcag agcagaaaacg gttggcctnt gtgttgcaac 60  
 cctcagcatc gcagtgccta tacgaattct gactacattc ctgatgggtg gtttcgctgg 120  
 cttaaacata aaggaaaaga tattttatttc ttttgcctgg cttccaaagg ccacggtcca 180  
 ggctgccatt ggctctgtgg ctctggacac ggcaagatcc cacggagaga agcagctgga 240  
 agactatggg atggatgtgc tgacgggtggc atttttggcc atcctcatta cagcaccaat 300  
 tggaagccta ctgattgggt tgctgggtcc cagggttctt cagaaatctg aacatcgaac 360  
 cgaagaggag gttcaaggag agacttctgc acacattcag aggaagcctg aggattccat 420  
 tacggaagcc tgatggacca tgtttaccat cccaacccaa aggttttggc cctccaacaa 480  
 ccgggacaac tttacttccc tttgactcag aagaaaactt cccgtggaat ttcataagca 540  
 aacaaattag aaagctttac gctgctaaca gtacctcagg tgtttacttc ctcaaaaaga 600



ccggaggaca ggttacttca gaaagtgaga gaaagtaatt tggacaaata aaacattcac	660
gattttgt	668